

Sequencing, Finishing and Analysis in the Future (SFAF)

La Fonda on the Plaza, Santa Fe, NM – June 2nd- 4th, 2010

Call for Abstracts (both talks and posters) Deadline March 30th, 2010

Please join us for the 5th annual "...in the Future" Meeting on Wednesday, June 2nd through Friday, June 4th in beautiful, historic Santa Fe, New Mexico. The three day SFAF conference will focus on how next generation sequencing data sets are shaping the field of Genomics in the areas of sequencing, assembly, finishing and analysis.

Keynote Speakers:

- Claire Fraser-Liggett, Ph.D., Director, Institute for Genome Sciences, Univ. of Maryland (UMSOM)
- Chad Nusbaum, Ph.D., Co-Director, Broad Institute Genome Sequencing and Analysis Program
- Folker Meyer, Ph.D., Associate Director, Institute for Genomics and Systems Biology, Argonne Natl. Lab

Areas to be emphasized include, but are not limited to the following:

Genome Sequencing:

- New sequencing technologies (454, illumina, SOLiD, Helicos, Pacific Biosciences, etc.)
- Draft sequencing strategies (prokaryotes, eukaryotes, metagenomics, single cell, etc.)
- *De novo* sequencing, re-sequencing, RNA sequencing, metagenomics, etc.

Genome Assembly:

- Whole genome assemblers and integration of next generation data
- *De novo* assemblers for short reads, hybrid assemblers
- Recalling and calibrating genome assemblies
- Single cell and metagenomic assemblies

Genome Finishing:

- Finishing systems and pipelines (automated, manual, etc.)
- Next generation finishing tools and technologies
- Quality standards for new technologies and mixed data sets
- Single cell / cell sorting and metagenomic finishing

Genome Analysis:

- Genome annotation and pathway identification tools and pipelines
- Comparative genomics, re-sequencing, SNPs, structural variation
- Large scale data management, cloud computing
- Metagenomic analysis



The conference is being sponsored and hosted by the DOE's Los Alamos National Laboratory and **NO** registration fee is required. Participants need to cover travel costs, hotel and dinner charges. Breakfast, lunch and snacks will be provided. A block of rooms are reserved at the La Fonda at a special conference rate of \$99 per night. **A limited number of extra rooms are available before & after the conference for those that want to stay in the area a little longer (contact Chris Detter for more details).**

Registration is limited to 120; please register soon if you plan to attend. **To register, submit an abstract, or obtain more information as it becomes available please visit our web site, <http://www.lanl.gov/finishinginthefuture/>. Registration will follow the same guidelines as in 2009 (see website).**

If you have any questions, or would like further information, please contact Chris Detter at (505)667-1326 or cdetter@lanl.gov.

We look forward to seeing you there!!!

The 2010 "Sequencing, Finishing and Analysis in the Future" Organizing Committee:



- * Chris Detter, Ph.D., JGI- LANL Center Director, LANL
- * Johar Ali, Ph.D., Cancer Genomics Team Leader, OICR
- * Patrick Chain, Metagenomics Team Leader, LANL
- * Michael Fitzgerald, Finishing Manager, Broad Institute
- * Bob Fulton, M.S., Sequence Improvement Group Leader, WashU
- * Darren Grafham, Finishing Coordinator, Sanger Institute
- * Jessica Hostetler, Genome Finishing and Analysis Manager, JCVI
- * Alla Lapidus, Ph.D., Finishing Coordinator / Group Leader, LBNL-JGI
- * Donna Muzny, M.S., Director of Operations, BCM

